学术动态ACADEMIC ACTIVITIES

我国启动重大入侵害虫苹果蠹蛾基因组测序

苹果蠹蛾 Cydia pomonella (L.)属鳞翅目卷蛾科,具有极强的适应性和抗逆能力,是仁果类果树的毁灭性害虫。1953 年首次在我国新疆库尔勒发现,并迅速扩散危害,1987 年随旅客携带物传入甘肃敦煌,造成了重大经济损失,是我国重点防控的检疫对象。近日,由中国农业科学院植物保护研究所、南京农业大学等科研单位联合启动了苹果蠹蛾的基因组测序工作。研究团队对苹果蠹蛾进行了 10 余代的纯化,建立了纯化品系。利用流式细胞分析和小片段文库前期测序等方法,对苹果蠹蛾基因组进行了初步的基因组前期分析。结果显示,苹果蠹蛾基因组大小约为 650 Mb, 17-mer 和 SNP 分析显示杂合度大约在 0.3% -0.6% 之间。经协商拟定了详细的全基因组鸟枪法测序方案后,基因组测序已经全面启动。苹果蠹蛾的基因组测序,对阐明其入侵机制、抗逆机理及防控等研究具有重要的推动意义。

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China launches a genome-sequencing project of the codling moth, *Cydia pomonella* (L.)

The codling moth, Cydia pomonella (L.) (Lepidoptera; Tortricidae), is a destructive insect pest in the fruit production. The occurrence of this notorious pest frequently causes huge economic loss to apple orchards. It also attacks pears, walnuts and other tree fruits. As one of the most important invasive species in China, the codling moth first appeared in Kuerle, Xinjiang in 1953 and rapidly expanded in the whole area of Xinjiang. In 1987 the codling moth spread to Dunhuang, Gansu. Recently, researchers from the Institute of Plant Protection of China Academy of Agricultural Sciences, Nanjing Agricultural University and so on initiated a genome-sequencing project of the codling moth. The genome size of the codling moth is 650 Mb as estimated by flow cytometry and survey sequencing. Since the heterozygosity is a potential obstacle in sequencing insect genome, the research consortium carefully measured the heterozygosity of the codling moth by SNP analysis and 17-mer estimation, showing that the heterozygosity of the codling moth is around 0.3% – 0.6%. Adopting the whole genome shotgun strategy, a sequencing plan has been made and officially launched. The availability of the codling moth genome should be of great value to uncovering the molecular mechanisms of its invasion and high adaptive ability to stress and developing efficient control strategies of this pest worldwide and in China.

Information source: Institute of Plant Protection, China Academy of Agricultural Sciences